

SEQUENCE LISTING

<110> GENSET S.A.

<120> USE OF PP2A PHOSPHATASE MODULATORS IN THE TREATMENT
OF MENTAL DISORDERS

<130> 794A WO

<150> US 60/391,359

<151> 2002-06-25

<160> 47

<170> PatentIn version 3.1

<210> 1

<211> 1932

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1)..(1932)

<223>

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 Glu Lys Lys Leu Lys Val Gly Phe Val Gly Leu Asp Pro Gly Ala Pro
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gac tcc acc cgg gac ggg gcg ctg ctg atc gcc ggc tcc gag gcc ccc 144
 Asp Ser Thr Arg Asp Gly Ala Leu Leu Ile Ala Gly Ser Glu Ala Pro
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aag cgc ggc agc atc ctc agc aaa cct cgc gcg ggc ggc gcg ggc gcc 192
 Lys Arg Gly Ser Ile Leu Ser Lys Pro Arg Ala Gly Gly Ala Gly Ala
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ggg aag ccc ccc aag cgc aac gcc ttc tac cgc aag ctg cag aat ttc 240
 Gly Lys Pro Pro Lys Arg Asn Ala Phe Tyr Arg Lys Leu Gln Asn Phe
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ctc tac aac gtg ctg gag cgg ccg cgc ggc tgg gcg ttc atc tac cac 288
 Leu Tyr Asn Val Leu Glu Arg Pro Arg Gly Trp Ala Phe Ile Tyr His
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gcc tac gtg ttc ctc ctg gtt ttc tcc tgc ctc gtg ctg tct gtg ttt 336
 Ala Tyr Val Phe Leu Leu Val Phe Ser Cys Leu Val Leu Ser Val Phe
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tcc acc atc aag gag tat gag aag agc tcg gag ggg gcc ctc tac atc 384
 Ser Thr Ile Lys Glu Tyr Glu Lys Ser Ser Glu Gly Ala Leu Tyr Ile
 115 120 125

ctg gaa atc gtg act atc gtg gtg ttt ggc gtg gag tac ttc gtg cgg 432
 Leu Glu Ile Val Thr Ile Val Val Phe Gly Val Glu Tyr Phe Val Arg
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 Ile Trp Ala Ala Gly Cys Cys Cys Arg Tyr Arg Gly Trp Arg Gly Arg
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ctc aag ttt gcc cgg aaa ccg ttc tgt gtg att gac atc atg gtg ctc 528
 Leu Lys Phe Ala Arg Lys Pro Phe Cys Val Ile Asp Ile Met Val Leu
 165 170 175

atc gcc tcc att gcg gtg ctg gcc gcc ggc tcc cag ggc aac gtc ttt 576
 Ile Ala Ser Ile Ala Val Leu Ala Ala Gly Ser Gln Gly Asn Val Phe
 180 185 190

gcc aca tct gcg ctc cgg agc ctg cgc ttc ctg cag att ctg cgg atg 624
 Ala Thr Ser Ala Leu Arg Ser Leu Arg Phe Leu Gln Ile Leu Arg Met
 195 200 205

atc cgc atg gac cgg cgg gga ggc acc tgg aag ctg ctg ggc tct gtg 672
 Ile Arg Met Asp Arg Arg Gly Gly Thr Trp Lys Leu Leu Gly Ser Val
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gtc tat gcc cac agc aag gag ctg gtc act gcc tgg tac atc ggc ttc 720
 Val Tyr Ala His Ser Lys Glu Leu Val Thr Ala Trp Tyr Ile Gly Phe
 225 230 235 240

ctt tgt ctc atc ctg gcc tcg ttc ctg gtg tac ttg gca gag aag ggg 768
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 245 250 255

gag aac gac cac ttt gac acc tac gcg gat gca ctc tgg tgg ggc ctg 816
 Glu Asn Asp His Phe Asp Thr Tyr Ala Asp Ala Leu Trp Trp Gly Leu
 260 265 270

atc acg ctg acc acc att ggc tac ggg gac aag tac ccc cag acc tgg 864
 Ile Thr Leu Thr Thr Ile Gly Tyr Gly Asp Lys Tyr Pro Gln Thr Trp
 275 280 285

aac ggc agg ctc ctt gcg gca acc ttc acc ctc atc ggt gtc tcc ttc 912

Asn Gly Arg Leu Leu Ala Ala Thr Phe Thr Leu Ile Gly Val Ser Phe
 290 295 300

ttc gcg ctg cct gca ggc atc ttg ggg tct ggg ttt gcc ctg aag gtt 960
 Phe Ala Leu Pro Ala Gly Ile Leu Gly Ser Gly Phe Ala Leu Lys Val
 305 310 315 320

cag gag cag cac agg cag aag cac ttt gag aag agg cgg aac ccg gca 1008
 Gln Glu Gln His Arg Gln Lys His Phe Glu Lys Arg Arg Asn Pro Ala
 325 330 335

gca ggc ctg atc cag tcg gcc tgg aga ttc tac gcc acc aac ctc tcg 1056
 Ala Gly Leu Ile Gln Ser Ala Trp Arg Phe Tyr Ala Thr Asn Leu Ser
 340 345 350

cgc aca gac ctg cac tcc acg tgg cag tac tac gag cga acg gtc acc 1104
 Arg Thr Asp Leu His Ser Thr Trp Gln Tyr Tyr Glu Arg Thr Val Thr
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gtg ccc atg tac agt tcg caa act caa acc tac ggg gcc tcc aga ctt 1152
 Val Pro Met Tyr Ser Ser Gln Thr Gln Thr Tyr Gly Ala Ser Arg Leu
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 385 390 395 400

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aaa ggc agc ccg tgc aga ggg ccc ctg tgt gga tgc tgc ccc gga cgc 1296
 Lys Gly Ser Pro Cys Arg Gly Pro Leu Cys Gly Cys Cys Pro Gly Arg
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ggc gtg gct gcc aag ggg aag ggg tcc ccg cag gcc cag act gtg agg 1392
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cgg tca ccc agc gcc gac cag agc ctc gag gac agc ccc agc aag gtg 1440
 Arg Ser Pro Ser Ala Asp Gln Ser Leu Glu Asp Ser Pro Ser Lys Val
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ccc aag agc tgg agc ttc ggg gac cgc agc cgg gca cgc cag gct ttc 1488
 Pro Lys Ser Trp Ser Phe Gly Asp Arg Ser Arg Ala Arg Gln Ala Phe
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cgc atc aag ggt gcc gcg tca cgg cag aac tca gaa gaa gca agc ctc 1536
 Arg Ile Lys Gly Ala Ala Ser Arg Gln Asn Ser Glu Glu Ala Ser Leu
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 Pro Gly Glu Asp Ile Val Asp Asp Lys Ser Cys Pro Cys Glu Phe Val
 515 520 525

acc gag gac ctg acc ccg ggc ctc aaa gtc agc atc aga gcc gtg tgt 1632
 Thr Glu Asp Leu Thr Pro Gly Leu Lys Val Ser Ile Arg Ala Val Cys
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gtc atg cgg ttc ctg gtg tcc aag cgg aag ttc aag gag agc ctg cgg 1680
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 545 550 555 560

ccc tac gac gtg atg gac gtc atc gag cag tac tca gcc ggc cac ctg 1728
 Pro Tyr Asp Val Met Asp Val Ile Glu Gln Tyr Ser Ala Gly His Leu
 565 570 575

gac atg ctg tcc cga att aag agc ctg cag tcc agg caa gag ccc cgc 1776
 Asp Met Leu Ser Arg Ile Lys Ser Leu Gln Ser Arg Gln Glu Pro Arg
 580 585 590

ctg cct gtc cag cag ggg aca aga acg ggg tgg gct tct ggg aca aag 1824
 Leu Pro Val Gln Gln Gly Thr Arg Thr Gly Trp Ala Ser Gly Thr Lys
 595 600 605

ccc act gtg gcc cat ggt ggg agt gca ggg ggt gtg tgg gcg ggg cct 1872
 Pro Thr Val Ala His Gly Gly Ser Ala Gly Gly Val Trp Ala Gly Pro
 610 615 620

cct ccc cac cca cgt cgg cct ctg tca gct tct gtt gtg tct tca caa 1920
 Pro Pro His Pro Arg Arg Pro Leu Ser Ala Ser Val Val Ser Ser Gln
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<212> PRT

<213> Homo sapiens

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Asp Ser Thr Arg Asp Gly Ala Leu Leu Ile Ala Gly Ser Glu Ala Pro
35 40 45

Lys Arg Gly Ser Ile Leu Ser Lys Pro Arg Ala Gly Gly Ala Gly Ala
50 55 60

Gly Lys Pro Pro Lys Arg Asn Ala Phe Tyr Arg Lys Leu Gln Asn Phe
65 70 75 80

Leu Tyr Asn Val Leu Glu Arg Pro Arg Gly Trp Ala Phe Ile Tyr His
85 90 95

Ala Tyr Val Phe Leu Leu Val Phe Ser Cys Leu Val Leu Ser Val Phe
100 105 110

Ser Thr Ile Lys Glu Tyr Glu Lys Ser Ser Glu Gly Ala Leu Tyr Ile
115 120 125

Leu Glu Ile Val Thr Ile Val Val Phe Gly Val Glu Tyr Phe Val Arg
130 135 140

Ile Trp Ala Ala Gly Cys Cys Cys Arg Tyr Arg Gly Trp Arg Gly Arg
145 150 155 160

Leu Lys Phe Ala Arg Lys Pro Phe Cys Val Ile Asp Ile Met Val Leu
165 170 175

Ile Ala Ser Ile Ala Val Leu Ala Ala Gly Ser Gln Gly Asn Val Phe
180 185 190

Ala Thr Ser Ala Leu Arg Ser Leu Arg Phe Leu Gln Ile Leu Arg Met
195 200 205

Ile Arg Met Asp Arg Arg Gly Gly Thr Trp Lys Leu Leu Gly Ser Val
210 215 220

Val Tyr Ala His Ser Lys Glu Leu Val Thr Ala Trp Tyr Ile Gly Phe
225 230 235 240

Leu Cys Leu Ile Leu Ala Ser Phe Leu Val Tyr Leu Ala Glu Lys Gly
245 250 255

Glu Asn Asp His Phe Asp Thr Tyr Ala Asp Ala Leu Trp Trp Gly Leu
260 265 270

Ile Thr Leu Thr Thr Ile Gly Tyr Gly Asp Lys Tyr Pro Gln Thr Trp
275 280 285

Asn Gly Arg Leu Leu Ala Ala Thr Phe Thr Leu Ile Gly Val Ser Phe
290 295 300

Phe Ala Leu Pro Ala Gly Ile Leu Gly Ser Gly Phe Ala Leu Lys Val
305 310 315 320

Gln Glu Gln His Arg Gln Lys His Phe Glu Lys Arg Arg Asn Pro Ala
325 330 335

Ala Gly Leu Ile Gln Ser Ala Trp Arg Phe Tyr Ala Thr Asn Leu Ser
340 345 350

Arg Thr Asp Leu His Ser Thr Trp Gln Tyr Tyr Glu Arg Thr Val Thr
355 360 365

Val Pro Met Tyr Ser Ser Gln Thr Gln Thr Tyr Gly Ala Ser Arg Leu
370 375 380

Ile Pro Pro Leu Asn Gln Leu Glu Leu Leu Arg Asn Leu Lys Ser Lys
385 390 395 400

Ser Gly Leu Ala Phe Arg Lys Asp Pro Pro Pro Glu Pro Ser Pro Ser

405 410 415

Lys Gly Ser Pro Cys Arg Gly Pro Leu Cys Gly Cys Cys Pro Gly Arg
420 425 430

Ser Ser Gln Lys Val Ser Leu Lys Asp Arg Val Phe Ser Ser Pro Arg
435 440 445

Gly Val Ala Ala Lys Gly Lys Gly Ser Pro Gln Ala Gln Thr Val Arg
450 455 460

Arg Ser Pro Ser Ala Asp Gln Ser Leu Glu Asp Ser Pro Ser Lys Val
465 470 475 480

Pro Lys Ser Trp Ser Phe Gly Asp Arg Ser Arg Ala Arg Gln Ala Phe
485 490 495

Arg Ile Lys Gly Ala Ala Ser Arg Gln Asn Ser Glu Glu Ala Ser Leu
500 505 510

Pro Gly Glu Asp Ile Val Asp Asp Lys Ser Cys Pro Cys Glu Phe Val
515 520 525

Thr Glu Asp Leu Thr Pro Gly Leu Lys Val Ser Ile Arg Ala Val Cys
530 535 540

Val Met Arg Phe Leu Val Ser Lys Arg Lys Phe Lys Glu Ser Leu Arg
545 550 555 560

Pro Tyr Asp Val Met Asp Val Ile Glu Gln Tyr Ser Ala Gly His Leu
565 570 575

Asp Met Leu Ser Arg Ile Lys Ser Leu Gln Ser Arg Gln Glu Pro Arg
580 585 590

Leu Pro Val Gln Gln Gly Thr Arg Thr Gly Trp Ala Ser Gly Thr Lys
595 600 605

Pro Thr Val Ala His Gly Gly Ser Ala Gly Gly Val Trp Ala Gly Pro
 610 615 620

Pro Pro His Pro Arg Arg Pro Leu Ser Ala Ser Val Val Ser Ser Gln
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Ser Leu Phe

<210> 3

<211> 1878

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1)..(1878)

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 Glu Lys Lys Leu Lys Val Gly Phe Val Gly Leu Asp Pro Gly Ala Pro
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gac tcc acc cgg gac ggg gcg ctg ctg atc gcc ggc tcc gag gcc ccc 144
 Asp Ser Thr Arg Asp Gly Ala Leu Leu Ile Ala Gly Ser Glu Ala Pro
 35 40 45

aag cgc ggc agc atc ctc agc aaa cct cgc gcg ggc ggc gcg ggc gcc 192
 Lys Arg Gly Ser Ile Leu Ser Lys Pro Arg Ala Gly Gly Ala Gly Ala
 50 55 60

ggg aag ccc ccc aag cgc aac gcc ttc tac cgc aag ctg cag aat ttc 240
 Gly Lys Pro Pro Lys Arg Asn Ala Phe Tyr Arg Lys Leu Gln Asn Phe
 65 70 75 80

ctc tac aac gtg ctg gag cgg ccg cgc ggc tgg gcg ttc atc tac cac 288
 Leu Tyr Asn Val Leu Glu Arg Pro Arg Gly Trp Ala Phe Ile Tyr His
 85 90 95

gcc tac gtg ttc ctc ctg gtt ttc tcc tgc ctc gtg ctg tct gtg ttt 336
 Ala Tyr Val Phe Leu Leu Val Phe Ser Cys Leu Val Leu Ser Val Phe

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 ctg gaa atc gtg act atc gtg gtg ttt ggc gtg gag tac ttc gtg cgg 432
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 130 135 140
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 Ile Trp Ala Ala Gly Cys Cys Cys Arg Tyr Arg Gly Trp Arg Gly Arg
 145 150 155 160
 ctc aag ttt gcc cgg aaa ccg ttc tgt gtg att gac atc atg gtg ctc 528
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 atc gcc tcc att gcg gtg ctg gcc gcc ggc tcc cag ggc aac gtc ttt 576
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 gcc aca tct gcg ctc cgg agc ctg cgc ttc ctg cag att ctg cgg atg 624
 Ala Thr Ser Ala Leu Arg Ser Leu Arg Phe Leu Gln Ile Leu Arg Met
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 atc cgc atg gac cgg cgg gga ggc acc tgg aag ctg ctg ggc tct gtg 672
 Ile Arg Met Asp Arg Arg Gly Gly Thr Trp Lys Leu Leu Gly Ser Val
 210 215 220
 gtc tat gcc cac agc aag gag ctg gtc act gcc tgg tac atc ggc ttc 720
 Val Tyr Ala His Ser Lys Glu Leu Val Thr Ala Trp Tyr Ile Gly Phe
 225 230 235 240
 ctt tgt ctc atc ctg gcc tcg ttc ctg gtg tac ttg gca gag aag ggg 768
 Leu Cys Leu Ile Leu Ala Ser Phe Leu Val Tyr Leu Ala Glu Lys Gly
 245 250 255
 gag aac gac cac ttt gac acc tac gcg gat gca ctc tgg tgg ggc ctg 816
 Glu Asn Asp His Phe Asp Thr Tyr Ala Asp Ala Leu Trp Trp Gly Leu
 260 265 270
 atc acg ctg acc acc att ggc tac ggg gac aag tac ccc cag acc tgg 864
 Ile Thr Leu Thr Thr Ile Gly Tyr Gly Asp Lys Tyr Pro Gln Thr Trp
 275 280 285
 aac ggc agg ctc ctt gcg gca acc ttc acc ctc atc ggt gtc tcc ttc 912
 Asn Gly Arg Leu Leu Ala Ala Thr Phe Thr Leu Ile Gly Val Ser Phe
 290 295 300

ttc gcg ctg cct gca ggc atc ttg ggg tct ggg ttt gcc ctg aag gtt 960
 Phe Ala Leu Pro Ala Gly Ile Leu Gly Ser Gly Phe Ala Leu Lys Val
 305 310 315 320

cag gag cag cac agg cag aag cac ttt gag aag agg cgg aac ccg gca 1008
 Gln Glu Gln His Arg Gln Lys His Phe Glu Lys Arg Arg Asn Pro Ala
 325 330 335

gca ggc ctg atc cag tcg gcc tgg aga ttc tac gcc acc aac ctc tcg 1056
 Ala Gly Leu Ile Gln Ser Ala Trp Arg Phe Tyr Ala Thr Asn Leu Ser
 340 345 350

cgc aca gac ctg cac tcc acg tgg cag tac tac gag cga acg gtc acc 1104
 Arg Thr Asp Leu His Ser Thr Trp Gln Tyr Tyr Glu Arg Thr Val Thr
 355 360 365

gtg ccc atg tac agt tcg caa act caa acc tac ggg gcc tcc aga ctt 1152
 Val Pro Met Tyr Ser Ser Gln Thr Gln Thr Tyr Gly Ala Ser Arg Leu
 370 375 380

atc ccc ccg ctg aac cag ctg gag ctg ctg agg aac ctc aag agt aaa 1200
 Ile Pro Pro Leu Asn Gln Leu Glu Leu Leu Arg Asn Leu Lys Ser Lys
 385 390 395 400

tct gga ctc gct ttc agg aag gac ccc ccg ccg gag ccg tct cca agc 1248
 Ser Gly Leu Ala Phe Arg Lys Asp Pro Pro Pro Glu Pro Ser Pro Ser
 405 410 415

cag aag gtc agt ttg aaa gat cgt gtc ttc tcc agc ccc cga ggc gtg 1296
 Gln Lys Val Ser Leu Lys Asp Arg Val Phe Ser Ser Pro Arg Gly Val
 420 425 430

gct gcc aag ggg aag ggg tcc ccg cag gcc cag act gtg agg cgg tca 1344
 Ala Ala Lys Gly Lys Gly Ser Pro Gln Ala Gln Thr Val Arg Arg Ser
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ccc agc gcc gac cag agc ctc gag gac agc ccc agc aag gtg ccc aag 1392
 Pro Ser Ala Asp Gln Ser Leu Glu Asp Ser Pro Ser Lys Val Pro Lys
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 Lys Gly Ala Ala Ser Arg Gln Asn Ser Glu Glu Ala Ser Leu Pro Gly
 485 490 495

gag gac att gtg gat gac aag agc tgc ccc tgc gag ttt gtg acc gag 1536
 Glu Asp Ile Val Asp Asp Lys Ser Cys Pro Cys Glu Phe Val Thr Glu

500 505 510

gac ctg acc cgg ggc ctc aaa gtc agc atc aga gcc gtg tgt gtc atg 1584
Asp Leu Thr Pro Gly Leu Lys Val Ser Ile Arg Ala Val Cys Val Met
515 520 525

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Arg Phe Leu Val Ser Lys Arg Lys Phe Lys Glu Ser Leu Arg Pro Tyr
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gac gtg atg gac gtc atc gag cag tac tca gcc ggc cac ctg gac atg 1680
Asp Val Met Asp Val Ile Glu Gln Tyr Ser Ala Gly His Leu Asp Met
545 550 555 560

ctg tcc cga att aag agc ctg cag tcc agg caa gag ccc cgc ctg cct 1728
Leu Ser Arg Ile Lys Ser Leu Gln Ser Arg Gln Glu Pro Arg Leu Pro
565 570 575

gtc cag cag ggg aca aga acg ggg tgg gct tct ggg aca aag ccc act 1776
Val Gln Gln Gly Thr Arg Thr Gly Trp Ala Ser Gly Thr Lys Pro Thr
580 585 590

gtg gcc cat ggt ggg agt gca ggg ggt gtg tgg gcg ggg cct cct ccc 1824
Val Ala His Gly Gly Ser Ala Gly Gly Val Trp Ala Gly Pro Pro Pro
595 600 605

cac cca cgt cgg cct ctg tca gct tct gtt gtg tct tca caa agt ctg 1872
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Phe
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<210> 4
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<213> Homo sapiens

<400> 4

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Asp Ser Thr Arg Asp Gly Ala Leu Leu Ile Ala Gly Ser Glu Ala Pro
35 40 45

Lys Arg Gly Ser Ile Leu Ser Lys Pro Arg Ala Gly Gly Ala Gly Ala
50 55 60

Gly Lys Pro Pro Lys Arg Asn Ala Phe Tyr Arg Lys Leu Gln Asn Phe
65 70 75 80

Leu Tyr Asn Val Leu Glu Arg Pro Arg Gly Trp Ala Phe Ile Tyr His
85 90 95

Ala Tyr Val Phe Leu Leu Val Phe Ser Cys Leu Val Leu Ser Val Phe
100 105 110

Ser Thr Ile Lys Glu Tyr Glu Lys Ser Ser Glu Gly Ala Leu Tyr Ile
115 120 125

Leu Glu Ile Val Thr Ile Val Val Phe Gly Val Glu Tyr Phe Val Arg
130 135 140

Ile Trp Ala Ala Gly Cys Cys Cys Arg Tyr Arg Gly Trp Arg Gly Arg
145 150 155 160

Leu Lys Phe Ala Arg Lys Pro Phe Cys Val Ile Asp Ile Met Val Leu
165 170 175

Ile Ala Ser Ile Ala Val Leu Ala Ala Gly Ser Gln Gly Asn Val Phe
180 185 190

Ala Thr Ser Ala Leu Arg Ser Leu Arg Phe Leu Gln Ile Leu Arg Met
195 200 205

Ile Arg Met Asp Arg Arg Gly Gly Thr Trp Lys Leu Leu Gly Ser Val
210 215 220

Val Tyr Ala His Ser Lys Glu Leu Val Thr Ala Trp Tyr Ile Gly Phe
225 230 235 240

Leu Cys Leu Ile Leu Ala Ser Phe Leu Val Tyr Leu Ala Glu Lys Gly
245 250 255

Glu Asn Asp His Phe Asp Thr Tyr Ala Asp Ala Leu Trp Trp Gly Leu
260 265 270

Ile Thr Leu Thr Thr Ile Gly Tyr Gly Asp Lys Tyr Pro Gln Thr Trp
275 280 285

Asn Gly Arg Leu Leu Ala Ala Thr Phe Thr Leu Ile Gly Val Ser Phe
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Phe Ala Leu Pro Ala Gly Ile Leu Gly Ser Gly Phe Ala Leu Lys Val
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Gln Glu Gln His Arg Gln Lys His Phe Glu Lys Arg Arg Asn Pro Ala
325 330 335

Ala Gly Leu Ile Gln Ser Ala Trp Arg Phe Tyr Ala Thr Asn Leu Ser
340 345 350

Arg Thr Asp Leu His Ser Thr Trp Gln Tyr Tyr Glu Arg Thr Val Thr
355 360 365

Val Pro Met Tyr Ser Ser Gln Thr Gln Thr Tyr Gly Ala Ser Arg Leu
370 375 380

Ile Pro Pro Leu Asn Gln Leu Glu Leu Leu Arg Asn Leu Lys Ser Lys
385 390 395 400

Ser Gly Leu Ala Phe Arg Lys Asp Pro Pro Pro Glu Pro Ser Pro Ser
405 410 415

Gln Lys Val Ser Leu Lys Asp Arg Val Phe Ser Ser Pro Arg Gly Val
420 425 430

Ala Ala Lys Gly Lys Gly Ser Pro Gln Ala Gln Thr Val Arg Arg Ser
435 440 445

Pro Ser Ala Asp Gln Ser Leu Glu Asp Ser Pro Ser Lys Val Pro Lys
450 455 460

Ser Trp Ser Phe Gly Asp Arg Ser Arg Ala Arg Gln Ala Phe Arg Ile
465 470 475 480

Lys Gly Ala Ala Ser Arg Gln Asn Ser Glu Glu Ala Ser Leu Pro Gly
485 490 495

Glu Asp Ile Val Asp Asp Lys Ser Cys Pro Cys Glu Phe Val Thr Glu
500 505 510

Asp Leu Thr Pro Gly Leu Lys Val Ser Ile Arg Ala Val Cys Val Met
515 520 525

Arg Phe Leu Val Ser Lys Arg Lys Phe Lys Glu Ser Leu Arg Pro Tyr
530 535 540

Asp Val Met Asp Val Ile Glu Gln Tyr Ser Ala Gly His Leu Asp Met
545 550 555 560

Leu Ser Arg Ile Lys Ser Leu Gln Ser Arg Gln Glu Pro Arg Leu Pro
565 570 575

Val Gln Gln Gly Thr Arg Thr Gly Trp Ala Ser Gly Thr Lys Pro Thr
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595 600 605

His Pro Arg Arg Pro Leu Ser Ala Ser Val Val Ser Ser Gln Ser Leu
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Phe
625

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 Glu Lys Lys Leu Lys Val Gly Phe Val Gly Leu Asp Pro Gly Ala Pro
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 gac tcc acc cgg gac ggg gcg ctg ctg atc gcc ggc tcc gag gcc ccc 144
 Asp Ser Thr Arg Asp Gly Ala Leu Leu Ile Ala Gly Ser Glu Ala Pro
 35 40 45
 aag cgc ggc agc atc ctc agc aaa cct cgc gcg ggc ggc gcg ggc gcc 192
 Lys Arg Gly Ser Ile Leu Ser Lys Pro Arg Ala Gly Gly Ala Gly Ala
 50 55 60
 ggg aag ccc ccc aag cgc aac gcc ttc tac cgc aag ctg cag aat ttc 240
 Gly Lys Pro Pro Lys Arg Asn Ala Phe Tyr Arg Lys Leu Gln Asn Phe
 65 70 75 80
 ctc tac aac gtg ctg gag cgg ccg cgc ggc tgg gcg ttc atc tac cac 288
 Leu Tyr Asn Val Leu Glu Arg Pro Arg Gly Trp Ala Phe Ile Tyr His
 85 90 95
 gcc tac gtg ttc ctc ctg gtt ttc tcc tgc ctc gtg ctg tct gtg ttt 336
 Ala Tyr Val Phe Leu Leu Val Phe Ser Cys Leu Val Leu Ser Val Phe
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 Ser Thr Ile Lys Glu Tyr Glu Lys Ser Ser Glu Gly Ala Leu Tyr Ile
 115 120 125
 ctg gaa atc gtg act atc gtg gtg ttt ggc gtg gag tac ttc gtg cgg 432
 Leu Glu Ile Val Thr Ile Val Val Phe Gly Val Glu Tyr Phe Val Arg
 130 135 140
 atc tgg gcc gca ggc tgc tgc tgc cgg tac cgt ggc tgg agg ggg cgg 480

Ile Trp Ala Ala Gly Cys Cys Cys Arg Tyr Arg Gly Trp Arg Gly Arg
 145 150 155 160

ctc aag ttt gcc cgg aaa ccg ttc tgt gtg att gac atc atg gtg ctc 528
 Leu Lys Phe Ala Arg Lys Pro Phe Cys Val Ile Asp Ile Met Val Leu
 165 170 175

atc gcc tcc att gcg gtg ctg gcc gcc ggc tcc cag ggc aac gtc ttt 576
 Ile Ala Ser Ile Ala Val Leu Ala Ala Gly Ser Gln Gly Asn Val Phe
 180 185 190

gcc aca tct gcg ctc cgg agc ctg cgc ttc ctg cag att ctg cgg atg 624
 Ala Thr Ser Ala Leu Arg Ser Leu Arg Phe Leu Gln Ile Leu Arg Met
 195 200 205

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cccaccag c gtc atc atg acc ggg gcc tac aac aac ttc ttc cgc atg 151355
 Val Ile Met Thr Gly Ala Tyr Asn Asn Phe Phe Arg Met
 355 360

ttc gat cgg aac acc aag cgg gac gtg acc ctg gag gcc tog agg gaa 151403
 Phe Asp Arg Asn Thr Lys Arg Asp Val Thr Leu Glu Ala Ser Arg Glu
 365 370 375 380

agc agc aag ccc cgg gct gtg ctc aag cca cgg cgc gtg tgc gtg ggg 151451
 Ser Ser Lys Pro Arg Ala Val Leu Lys Pro Arg Arg Val Cys Val Gly
 385 390 395

ggc aag cgc cgg cgt gat gac atc agt gtg gac agc ttg gac ttc acc 151499
 Gly Lys Arg Arg Arg Asp Asp Ile Ser Val Asp Ser Leu Asp Phe Thr
 400 405 410

aag aag atc ctg cac acg gcc tgg cac cgg gct gag aac atc att gcc 151547
 Lys Lys Ile Leu His Thr Ala Trp His Pro Ala Glu Asn Ile Ile Ala
 415 420 425

atc gcc gcc acc aac aac ctg tac atc ttc cag gac aag gta aac tct 151595
 Ile Ala Ala Thr Asn Asn Leu Tyr Ile Phe Gln Asp Lys Val Asn Ser
 430 435 440

gac atg cac tag g tatgtgcagt tcccgcccc tgccaccag cctcatgcaa 151648
 Asp Met His
 445

gtcatccccg acatgacctt cagcaccgca atgcaaggag gggaagaaag tcacagcact 151708

gatgaggaca gctgcagagg tggcagtgtg tggacacagg aagtttgggc cccctccctg 151768

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<212> PRT

<213> Homo sapiens

<400> 38

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Asp His Ser Tyr Val Thr Glu Ala Asp Ile Ile Ser Thr Val Glu Phe
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Asn His Thr Gly Glu Leu Leu Ala Thr Gly Asp Lys Gly Gly Arg Val
35 40 45

Val Ile Phe Gln Arg Glu Pro Glu Ser Lys Asn Ala Pro His Ser Gln
50 55 60

Gly Asp Tyr Asp Val Tyr Ser Thr Phe Gln Ser His Glu Pro Glu Phe
65 70 75 80

Asp Tyr Leu Lys Ser Leu Glu Ile Glu Glu Lys Ile Asn Lys Ile Lys
85 90 95

Trp Leu Pro Gln Gln Asn Ala Ala His Ser Leu Leu Ser Thr Asn Asp
100 105 110

Lys Thr Ile Lys Leu Trp Lys Ile Thr Glu Arg Asp Lys Arg Pro Glu
115 120 125

Gly Tyr Asn Leu Lys Asp Glu Glu Gly Lys Leu Lys Asp Leu Ser Thr
130 135 140

Val Thr Ser Leu Gln Val Pro Val Leu Lys Pro Met Asp Leu Met Val
145 150 155 160

Glu Val Ser Pro Arg Arg Ile Phe Ala Asn Gly His Thr Tyr His Ile
165 170 175

Asn Ser Ile Ser Val Asn Ser Asp Cys Glu Thr Tyr Met Ser Ala Asp
180 185 190

Asp Leu Arg Ile Asn Leu Trp His Leu Ala Ile Thr Asp Arg Ser Phe
195 200 205

Asn Ile Val Asp Ile Lys Pro Ala Asn Met Glu Asp Leu Thr Glu Val
210 215 220

Ile Thr Ala Ser Glu Phe His Pro His His Cys Asn Leu Phe Val Tyr
225 230 235 240

Ser Ser Ser Lys Gly Ser Leu Arg Leu Cys Asp Met Pro Ala Ala Ala
245 250 255

Leu Cys Asp Lys His Ser Lys Leu Phe Glu Glu Pro Glu Asp Pro Ser
260 265 270

Asn Arg Ser Phe Phe Ser Glu Ile Ile Ser Ser Val Ser Asp Val Lys
275 280 285

Phe Ser His Ser Asp Arg Tyr Met Leu Thr Arg Asp Tyr Leu Thr Val
290 295 300

Lys Val Trp Asp Leu Asn Met Glu Ala Arg Pro Ile Glu Thr Tyr Gln
305 310 315 320

Val His Asp Tyr Leu Arg Ser Lys Leu Cys Ser Leu Tyr Glu Asn Asp
325 330 335

Cys Ile Phe Asp Lys Phe Glu Cys Ala Trp Asn Gly Ser Asp Ser Val
340 345 350

Ile Met Thr Gly Ala Tyr Asn Asn Phe Phe Arg Met Phe Asp Arg Asn
355 360 365

Thr Lys Arg Asp Val Thr Leu Glu Ala Ser Arg Glu Ser Ser Lys Pro
370 375 380

Arg Ala Val Leu Lys Pro Arg Arg Val Cys Val Gly Gly Lys Arg Arg
385 390 395 400

Arg Asp Asp Ile Ser Val Asp Ser Leu Asp Phe Thr Lys Lys Ile Leu
405 410 415

His Thr Ala Trp His Pro Ala Glu Asn Ile Ile Ala Ile Ala Ala Thr
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Asn Asn Leu Tyr Ile Phe Gln Asp Lys Val Asn Ser Asp Met His
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<210> 40

<211> 19

<212> DNA

<213> Artificial

<220>

<223> primer 24-257/320

<400> 40

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<210> 41

<211> 19

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<223> primer 99-24175/218

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<210> 42

<211> 601

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tgccggtctc caccggcccc acgggcaccg tgccaatgcc tgcagagggg aggggggtgtg 180
aggggaaggt ggggcccag gggatgctgg ggcaggatat tcggggacag agcctggaaa 240
ccaacaaagc ctgggactgg atcccccca caggcctggg ggttggggcc acatgggcgg 300
rgtgcagggg aaggagggcc agggacaagg gcagacacag agattccaag ggaagtgggg 360
gtctccac ccagctgggg aaataagagg ctgagcagca gagctcccag gaaccacgg 420
aaaagccaca gggacagaga agcgggagga tgggcagaga ggggctgtct gaacctgggg 480
tccatcctt gccccggag agcactttcc ctcaaaggag gcactatggg acccctcctt 540
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<211> 601
<212> DNA
<213> Artificial

<220>
<223> amplicon 30-2

<220>
<221> allele
<222> (301)..(301)
<223> biallelic marker 30-2/62

<400> 43

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 tgtgtggggg cagggggccct gctgacttag aaacaagtgg cacattgatc cgattcaaa 180
 cttgccagcc aatcaaccac agccccgcgc acagactctc ccaggtggga ctgaggggggt 240
 ctccctgtc cttggcaggg gcgtctcccc cagcacccc cagtccgctc ctctccacag 300
 rctccagatg cccacatccc cagaacactc aatgggacaa ctgagagcag gttacagaga 360
 aagaaaagcc acacaagctc accaagggca cgctattca gaagtgcctt ctctctctgg 420
 aatgtcgac cccaaagctc tctctgggaa acctctggcc tggccccggg aagcgacagg 480
 cgcaggtttg gggctgaggc cgtcccagca gctctgtggc ctgccagacc tcagagcact 540
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a

601

<210> 44

<211> 601

<212> DNA

<213> Artificial

<220>

<223> amplicon 30-17

<220>

<221> allele

<222> (301)..(301)

<223> biallelic marker 30-17/37

<400> 44

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 ctgtctccag ggatataggg gctggatgga cccgtctcct gaggccagca gaggtccac 120
 gccagggtcg gtggcagggc tggcacaggg gaaccaggag gcgccgctgg cttcaccatc 180
 ttagctacgg cagcccattc ccctgagcct cctggcctgg gcaacagtgg ctgcatggc 240
 cagcccaccg tgccctccag ggtcagtagc gtctattctg gcggccagca gggttgagga 300
 rtcttgggac tgttgagacc ctccccaac ctccctgagc ctccgggcac agatgtgaaa 360

agggtgcccc ctgcagtcag cactcaaccc ccacagcgtc caggaggagga gagggggccac 420
 cggggggctga cccctgcccc ttctgcagac aaagccacca ccctgccagg gctcaagagg 480
 gaagaaaatg gggaggggggc catttgagca aatgagcca cccgtgagca aggtggaggg 540
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<210> 45
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<220>
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<220>
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 <222> (301)..(301)
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 cgtgcccatg gggggccagg gtgctcagag tcctggtgct gtgggtgcct ctgtccaac 180
 ggcctctggt ccccatccca acaacaaaag cacagggtgt cgggggagaac cggacggggg 240
 ccaggggagc acatgggcac aggctcagcg ggactcctgg aatgttctct ctttctccac 300
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<220>
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<400> 46
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 agccttgaag gcactcattc actcacgcat cgggggctag tacaggctgt gacagaggcc 180
 tgagctggaa ctgtgacca ggacacacac atggccatgt ggcctctggg cttcctcaca 240
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 rtggatcctg gcctggcctt ggagtcaggc agtgtcactc ctgtgccttc taacctgggc 360
 ccccgggccc aaggggagga aatggagacc ccacctcca gtggagggaa ggcaaggtcc 420
 cactgtgggg gtagcacatg ggatacacc atgtggctgc cgctggagac gttagtttgc 480
 cacaccgtt tcttctacgt gaacatttgc ctgcatctca ctttctaact cctgggtgct 540
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<210> 47
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 <213> Artificial

<220>
 <223> amplicon 30-15

<220>
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 <222> (301)..(301)
 <223> biallelic marker 30-15/54

<400> 47

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cagggcccac caggggctca caggaaaggt cgtggaaaat tacaagaaat cttccctctg 180
gcactagcgg gtgaggggaa tggaagccac cgccagacag caccatctcc tcaccctcct 240
gtgaagcaca agactcactt gcagagggaa gagcgcagaa accgtcacc caggacgctg 300
mgggtgaacg agaggaagcg agaattggaga agccctggcc ctggggaaca g gatggaaaa 360
cgcttggtc agctccgtgg ctgcgaagga accggcgcgc tcgcggaggc cacaccccg a 420
gacccgagga cacagtgcct gcctgagatg gagccagaaa cattctccac ctttcacgc 480
aagactaaca agggctccat gaaaataaaa ctggaagagc tgaaagagaa gcattctccc 540
tgggtgtgaa accaagaaaa gacacaaagc caaggaaaag ccattgagaa aacacctggc 600

a

601